

First, a clarification about the Genetic Relationship and Fingerprinting (GRAF) software:

GRAF is a tool for researchers, it is not designed to assess an individual's ancestry or to find relatives.

GRAF is a downloadable C++ application, compiled for GNU/Linux. We use GRAF at NCBI as a quality assurance tool in dbGaP data processing. We're presenting this tool publicly so any researcher can check the quality of their own data. Another function of GRAF is for analyzing the genotype-based ancestry of subjects in Genome Wide Association Studies (GWAS).

For more information see:

- NCBI Blog post: <https://ncbiinsights.ncbi.nlm.nih.gov/2017/10/16/graf-new-tool-finds-duplicates-close-relatives-large-genomic-datasets-dbgap/>
- Publication: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5469481/>
- GRAF software download: <https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/Software.cgi>
- GRAF documentation from the software package:
https://ftp.ncbi.nlm.nih.gov/pub/education/public_webinars/2018/06Jun27_GRAF/

Q: How is it different from BLAST and FASTA?

A: Different purposes. GRAF is not an alignment tool.

Q: Is GRAF able to find relations between ancestors of specific time? for example - 100 years ago vs 200 years.

A: No.

Q: Can GRAF be downloaded on android?

A: Possibly. We have not tested this.

Q: How can we check the relationship by using this technique... Can u please elaborate?

A: You can only do this for genotype data, typically from genome-wide association studies (GWAS), such as that in dbGaP. Please refer to the GRAF documentation noted above.